

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 30, 2003, 02:51:12 ; Search time 1626.01 Seconds
(without alignments)
13446.329 Million cell updates/sec

Title: US-09-768-781-1

Perfect score: 1350

Sequence: 1 atggacagagtttatgaaat.....caaggcaaaagtgtgtctga 1350

Scoring table: IDENTITY NUC

Gapop 10⁻⁷, Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmv:*

5: em_estov:*

6: em_estpi:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	301.8	22.4	1711	11	AK007734 Mus muscu
2	293	21.7	1774	11	BC027097 Mus muscu
3	259.4	19.2	624	10	BB200527 Mus muscu
4	245.4	18.2	810	12	EG675952 EG675952
5	240.6	17.8	676	9	AL652777 AL652777
6	236.8	17.5	392	10	BE031611 BE031611

RESULT 1
AK007734
LOCUS
DEFINITION
Mus musculus 10 day old male pancreas cDNA, RIKEN full-length
enriched library, clone:1810038K19;McLeod syndrome gene homolog,
full insert sequence.
ACCESSION
AK007734
VERSION
AK007734.1 GI:12841469
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (strain:CS7BL/6J) 10 day old male pancreas cDNA to
mRNA, clone lib:RIKEN full-length enriched mouse cDNA library
clone:1810038K19.
ORGANISM
Mus musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636
REFERENCE
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374
PUBMED
11042159

ALIGNMENTS

7	198.8	14.7	881	13	BI827782
8	197.8	14.7	201	9	AA256009
9	193.4	14.3	678	9	AL638533
10	182.6	13.5	793	13	BI546216
11	173.2	12.8	385	9	AA791818
12	170.4	12.6	691	17	CNS032LV
13	164.6	12.2	855	13	BI463670
14	113.2	8.4	691	17	AG085155
15	107.6	8.0	666	13	BI461092
16	106	7.9	1035	17	CNS01TL3
17	102	7.6	346	14	HB7640
18	88.6	6.6	535	14	BM683941
19	88.6	6.6	537	14	BM931807
20	77.6	5.7	921	12	BF672674
21	73.2	5.4	447	9	AI697050
22	59.6	4.4	869	17	CNS032YG
23	56.8	4.2	387	17	AQ087397
24	56.2	4.2	694	10	BB638337
25	53	3.9	627	12	BF211581
26	49.8	3.7	574	17	AZ593746
27	49.4	3.7	550	10	BB611251
28	48.6	3.6	857	17	CNS03K4E
29	46.8	3.5	755	9	AL653785
30	46.2	3.4	930	14	BQ718536
31	43.4	3.2	431	10	AW374923
32	43.4	3.2	464	9	AI923193
33	43.4	3.2	588	9	AI831578
34	43.4	3.2	588	12	BF195029
35	43.4	3.2	589	14	BM842656
36	43.4	3.2	609	10	AW966092
37	43.4	3.2	886	13	BI753850
38	43.4	3.2	917	9	AL551219
39	43.4	3.2	922	9	AL556942
40	43.4	3.2	926	12	BE735816
41	43.4	3.2	993	13	BM472443
42	43.4	3.2	1009	9	AL547473
43	43.4	3.2	1042	13	BM470447
44	43.4	3.2	1149	13	BM466219
45	43.2	3.2	877	13	BI463669

BI827782 603075458
AA256009 282806.4
AL638533 AL638533
BI546216 603188602
AA791818 v861C09.f
AL202756 Tetraodon
BI463670 603207340
AG085155 Pan trogl
BI461092 603206970
AL166856 Tetraodon
HB7640 yw17911.r1
BM683941 UI-B-EJ1-
BM931807 UI-B-EJ1-
BF672674 602152274
AI697050 wc85d10.x
AL225457 Tetraodon
AQ087397 HS_2187.A
BB638337 BB638337
BF211581 601812270
AZ593746 IM0405N22
BB611251 BB611251
AL247703 Tetraodon
AL653785 AL653785
BQ718536 AGENCOURT
AW374923 MRO-CT006
AI923193 wt49d11.x
AI831578 wt39c11.x
BF195029 7091n12.x
BM842656 K-EST0120
AW966092 EST378165
BI753850 603027531
AL551219 AL551219
AL556942 AL556942
BE735816 601305125
BM472443 AGENCOURT
AL547473 AL547473
BM470447 AGENCOURT
BM466219 AGENCOURT
BI463669 603207339


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QY 535 GGCTCAGTGGCCAGCTGACCTATCAGCTCTATGTGAGCCTGATCTCTGCAGAGTTCC 594
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 595 CTGGGTAGAGTTGTCTAATGTTATTTTCCCTGGTATCTGTCACTATGCGGCCACCTT 654
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 705 ACTGGAAGATGCTTTCATCATGACCTTGTCCCTGTCTCTATTGTCTATGGCGCTTACGT 764
QY 655 TGAATATGTTGGCTATCCAGATCAAGTACGATGACTACAGATTCGCTTGGGCCACTA 714
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 765 TGAACATCTTAGCCATCAAAATCAAGTATGATGATGAGTCAAAAGTCAAAACCTG 824
QY 715 GAAGTCTCTGCACTCACCATCTGCGGACATCTGGAGATCACTTCCCGCTCTCTGATCTG 774
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 825 GCTTATGCTGTATCTCTCTGAGAGCTTTGAGATGGCCAGCTATGCTGCTG 884
QY 775 GTGCTCTTCTCAGCACCTTTGAAATGAAAGCTGTGCGCTTCTTAGTGTCTCAACTTCCTG 834
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 885 GTCTCTTTACCTCTGTCTCTGAAGATCTGGGTGGTGGCAGTCACTCTCAACTTCTTC 944
QY 835 ATCATCTCTTTGAGCCCTGATTAAGTTCTGGAGAGTGGTGGCCAGATGCCCAATTAAC 894
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 945 AGCTTCTTTATATCCCTGGATCGTTTCTGGTGCAGTGGCTCCCAATTCCTTGAGAAC 1004
QY 895 ATTGAGAAAACTTCAGCGGGTGGCACTCTGTGTGTCCTGATTTTCACTCACCATCTCTC 954
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1005 ATAGAGAAAGCCCTAAGTAGGCTGGTACCACTGCTGCTCTCTCTCTCACTTACTC 1064
QY 955 TATGCTGGCATCACTTCTCTTGTGCTGCTGAGCTTTTGCAGTTTGGAGTTGGCAGACAGAT 1014
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1065 TATGCGGCATCAATGTTCTGCTGGTGCAGTGTTCAGCTGAAATCGCAATCCGGAG 1124
QY 1015 CTGCTGACAAAGGGAGAACTGGGACATATGGCCCTGCACTATAGTGTGAGTTGGTA 1074
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1125 CTCATCAGCAAGTCCAGAACTGTGACCGCTGCTCACTTACTACATGACGAGATTCATC 1184
QY 1075 GAGATGTGATCATGGTCTGGTCTTTTAAAGTTCTTTGGAGTGAAGTGTACTGAATTAAC 1134
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1185 GAGAACTCCGCTCTCTGCTCTCTGTTATTTTAAAGTGAATATATGATGATG 1244
QY 1135 TGTCAATCTCTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1194
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1245 TGTGGCCCTCTGTTGATCTTGCAGCTGCTTATTTGGTACTGCACTGGCATCTCTTCTCATG 1304
QY 1195 CTCTTTTCTTCCAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1247
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1305 CTGTGTCTCTCATGTTTTCACCCCTTGCAAAAGCTCTTCTCTCTCAGTGT 1357
```

```
RESULT 2
BC027097 1774 bp mRNA linear HTC 07-AUG-2002
LOCUS Mus musculus, McLeod syndrome gene homolog, clone IMAGE:5012421,
DEFINITION mRNA
ACCESSION BC027097
VERSION BC027097.1 GI:20071516
KEYWORDS HTC.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1774)
Direct Submission
Submitted (04-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabbs-x@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
```

cdna Library Preparation: Life Technologies, Inc.
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gundaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 45 Row: d Column: 3
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 12963702
This clone has the following problem: frame shifted.

FEATURES

source

1. 1774
/location="Qualifiers"
/organism="Mus musculus"
/db_xref="taxon:10090"
/map="CZECHE II"
/clone="IMAGE:5012421"
/tissue_type="Mammary tumor metastasized to lung. Tumor
arose spontaneously from a senescent normal mammary
(clonal) outgrowth infected with the virus MMTV."
/clone_lib="NCI CGAP_Lu29"
/lab_hosts="DH10B"
/notes="vector: pCMV-SPORT6"
BASE COUNT 386 a 513 c 441 g 434 t
ORIGIN

Query Match 21.7%; Score 293; DB 11; Length 1774;
Best Local Similarity 55.6%; Pred. No. 7.9e-68;
Matches 630; Conservative 0; Mismatches 490; Indels 13; Gaps 3;
QY 118 TCCACCTTTTGTACTGTGGGGAGCTGCATCTGCTTGTATCATGTTAGTATCTATCGA 177
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 262 TCCGTGTCTCTGTTGTCGGCCGACGCGCGGCTCTACTTGGACGACCTACCGC 321
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 178 AAGAAATAGTAACTTACCGGATGACATACACCTTTCTTTTATGTTTTCATCCATT 237
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 322 TCCGACGGGACCGCATGTGCGAGTGTGAGCTGTCTTCTCTGATGCCCTGCGCC 381
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 238 ATGTCAGTTGACCTCATTTTGTCCACAGAGATCTAGCCAAAGATAAACCGCTATCA 297
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 382 CTGCTGCAAGTTCAGCTCTCTTCTGTCACCGCGACCTCAGCGCGATCGGCCACTGGCG 441
QY 298 TTATTATGATCTAATCTCTTGGGACCTGTTATCAGATGTTTGGAGGCCATGATTAG 357
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 442 CTGCTCAGACCTGTCTCCAGCTCGGGCCCTGTACAGGTGTGTGAAAGTCTTTTGTATC 501
QY 358 TACCTCACACTGTGGAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 416
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 502 TAC-----TGTCACTCCGACCAAGATGAAGACCTTATGTGAGCATCACTAAGAA 552
QY 417 --GAAGATGCTAATAGATGGCGAGAGGTGCTGATAGAAATGGGAGGTGGCGCACTCCATC 474
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 553 CGACAGATGCCAAAGATGGCTTTTACAGAGAGGTGGGAGAAAGAGGTGGCGCAGCAAG 612
QY 475 CGGACCTTGGTATGACCCCAATGCCATCAAAAGTATGTACAGATCCAGACCTTCTG 534
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 613 GCGAAGTGTATACCCCGTCTTGCATTCAGCCGGGATCAGTGATACAGGCTTTCTC 672
QY 535 GGCTCAGTGGCCAGCTGACCTATCAGCTCTATGTGAGCCTGATCTCTGCAGAGGTTCC 594
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 673 GGCTCTGCCCACTGACCTTCACTGATATTAATCTGTTGGAGCAGAAATCACT 732
QY 595 CTGGGTAGAGTTGTGCTAATGTTATTTTCCCTGGTATCTGTCACTTGGGCGCACCTT 654
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 733 ACTGGAAGATGCTTCATCATGACCTTGTCTCTGCTGCTTATGTTATGGGCGCTTACGT 792
QY 655 TGCAATATGTTGGCTATCCAGATCAAGTACGATGACTCAAGATTCGCTTGGGCCACTA 714

QY 505 AACGTATGTACAGATCAAGCCTTCTGGCTCAGTGGCCAGCTGACCTATCAGCTC 564
 Db 181 AAACGTATGTACAGATTCAGCCTTCTGGCTCAGTGGCCAGCTGACCTATCAGCTA 240

QY 565 TATGTAGCCTGATCTCTGCAGAGGTTCCTCCCTGGGTAGAGTTGTG 609
 Db 241 TATGTAGTCTGATCTCAGCAGAGTCCCTCCCTGGGTAGAGTTGAG 285

RESULT 4
 BG675952
 LOCUS 602623310F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4747323 5',
 DEFINITION mRNA sequence.
 ACCESSION BG675952
 VERSION BG675952.1 GI:13907348
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 810)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-i@mail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10597 row: c column: 04
 High quality sequence start: 4
 High quality sequence stop: 797.

FEATURES
 source
 1. 810
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4747323"
 /clone_lib="NCI_CGAP_Skn4"
 /tissue_type="squamous cell carcinoma"
 /lab_host="DH10B (TI phage-resistant)"
 /notes="Origin: skin; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 214 a 178 c 169 g 249 t
 ORIGIN
 Query Match 18.2%; Score 245.4; DB 12; Length 810;
 Best Local Similarity 99.2%; Pred. No. 4.2e-55;
 Matches 257; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1092 CTTGGTTTTAAGTCTTTGGAGTGAAGTGTACTGAATTAATCTGTCATTCCTTGATTCG 1151
 Db 1 CTTGGTTTTAAGTCTTTGGAGTGAAGTGTACTGAATTAATCTGTCATTCCTTGATTCG 60

QY 1152 CTTGCAGCTCATTTATGCTTATCTGATTTCCATTGATTCATGCTCCTTTTCTTCCAGTA 1211
 Db 61 CTTGCAGCTCATTTATGCTTATCTGATTTCCATTGATTCATGCTCCTTTTCTTCCAGTA 120

QY 1212 CTTGCATCAATTCGGCTCACTCTTCACCCCATATGTTAGTAGACTACCTCCATTTGTCTG 1271
 Db 121 CTTGCATCAATTCGGCTCACTCTTCACCCCATATGTTAGTAGACTACCTCCATTTGTCTG 180

QY 1272 CTTGTACACGACCCCTGGACCGGTTGAGACTCTAGAGCCACCTTTGAGACTGAAGC 1331
 Db 181 CTTGTACACGACCCCTGGACCA -GGTTGAGACTCAGAGCCACCTTTGAGACTGAAGC 239

QY 1332 AAGCCAAAGTGTGTCTGA 1350
 Db 240 AAGCCAAAGTGTGTCTGA 258

RESULT 5
 AL652777
 LOCUS AL652777 XGC-gastrula Silurana tropicalis cDNA clone Tgas029g15 5',
 DEFINITION mRNA sequence.
 ACCESSION AL652777
 VERSION AL652777.1 GI:17663442
 KEYWORDS EST.
 SOURCE western clawed frog.
 ORGANISM Silurana tropicalis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenopodinae; Silurana.
 REFERENCE 1 (bases 1 to 676)
 AUTHORS Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
 TITLE Sanger Xenopus tropicalis EST project 2001 (10_2001)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Huckle E
 Sanger Centre
 Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: tropesanger.ac.uk
 Sanger Xenopus tropicalis EST project 2001
 TROPICALIS SEQUENCE ID: Tgas029g15.sp6
 Sequencing primer: SP6
 This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn.
 Location/Qualifiers
 source
 1. 676
 /organism="Silurana tropicalis"
 /db_xref="taxon:8364"
 /clone="Tgas029g15"
 /clone_lib="XGC-gastrula"
 /dev_stage="gastrula (stages 10.5-13 mixed)"
 /lab_host="Escherichia coli XL1-blue"
 /notes="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
 was oligo dT primed from Sug of poly A+ RNA from stages
 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
 into pCS107 with EcoRI at the 5' end and NotI at the 3'
 end."

BASE COUNT 138 a 159 c 155 g 224 t
 ORIGIN
 Query Match 17.8%; Score 240.6; DB 9; Length 676;
 Best Local Similarity 59.9%; Pred. No. 7.8e-54;
 Matches 402; Conservative 0; Mismatches 269; Indels 0; Gaps 0;

QY 604 GTTGTGCTAATGTTATTTTCCTGGTATCTGTCACTATGGGCGCCACCTTTGCAATATG 663
 Db 6 GGTGTCTCATGGTATGTGTCTTGCCTCAACTACATATGTCCTTAATCCTAATATGC 65

QY 664 TTGCTATCCAGATCAAGTACGATGACTACAAGATTGCCTTGGGCCACTAGAAGTCTTC 723
 Db 66 CTGGCCATCAAAATTAAGTATGATGACTATAAAGTTCGTCTAAGTGGCCAGCGTTCTG 125

QY 724 TGCATACCATCTGGCCGACATTGGAGATCACTTTCCGCCCTCCTGATTCGGTGCCTTC 783
 Db 126 TGCATCGTATGGAGATGCTGGAGATTGCTACCGGTGTACAGATTCTGTTCTTTT 185

QY 784 TCAGCCACTTGAATTTGAAGGCTGTGCCCTTCTCTAGTGTCAACTCTCTCATCATCTC 843
 Db 186 TGTTCACTCTTAAAGCCTGGGTGGCTGCAGTGGCCCTTAGCAAACTTACTCGCGCTCTC 245

QY 844 TTTGAGCCCTGGATTAAGTTCTGGAGAAGTGGTCCAGATGCCCAATAAATAGAGAA 903
 Db 246 CTTTTCCTTTGGGTTAAATTTCTGAGCAGTGGGACACGCTGCCCCCAAAACATAGAAAG 305

QY 904 AACTTCAGCCGGGTGGCACTCTGGTGGTCTCTGATTTTCAGTCAACCATCTCTATGCTGC 963
 Db 904 AACTTCAGCCGGGTGGCACTCTGGTGGTCTCTGATTTTCAGTCAACCATCTCTATGCTGC 963

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Db 306 AACTTTAGCTGTTGGTACTGTGTACAGTCTTGGTGCAGTAACCTTGCTTTATTACGCC 365
Qy 964 ATCAACTTCTCTTGTCTGCTCAGCTTTGAGTTGGAGTGGGACAGACAGATCTGCTGCAC 1023
Db 366 ATCAATATGTTTCTGCTGCTGCTGCTTACAGTAAACCTATCAGATCGGACCTTAATGAC 425
Qy 1024 AAGGGCAGAACTGGGACATATGGGCCCTGCACTATAGTGTGAGGTTGGTAGAGAAATGTG 1083
Db 426 CAGTCACAAAACCTGGGGAGGTTAAGTCTTCAATTATACCATTCGCGTTGCTCGAGAATGCA 485
Qy 1084 ATCATGCTCTGTTTAAAGTTCTTTGGAGTGAAGTGTCTACTGAATTAATCTGCTCAATCC 1143
Db 486 GCCCTCATCTGCTCTGCTGCTTCTACAGGAGGATGTTTGGATATTTCTTGTTCCCA 545
Qy 1144 TTGATTGCTTGGCAGCTCATTTATCTTATCTGATTTTCCATTGACTTCAATGCTCTCTTTC 1203
Db 546 CTGCTGGTGTCAACTCTTAGTAGATATGCCCGCCATCTTCTTATGCTGCTTTT 605
Qy 1204 TTCAGTACTTGCATCCATTCCTGCTCACTCTTCCACCCATAATGTAGTAGACTACCTCCAT 1263
Db 606 TACCAGTACCTTCACCTTGGCGCTTCTCTTTCAGCCACAGGTTGAAGACTGTTTGGCT 665
Qy 1264 TGTGCTGCTG 1274
Db 666 TGTGTTGCTG 676

RESULT 6
LOCUS BE031611 392 bp mRNA linear EST 09-JUL-2000
DEFINITION 130228 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BE031611
VERSION BE031611.1 GI:8326620
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 392)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.,
and Keefe, J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
JOURNAL EST discovery in swine
COMMENT Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCACAGTACGACG
Plate: 59 row: C column: 17
Seq primer: ATTTAGGTGACACTATAG.
FEATURES
Location/Qualifiers
1..392
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 81 a 87 c 100 g 124 t
ORIGIN

Query Match 17.5%; Score 236.8; DB 10; Length 392;
Best Local Similarity 57.3%; Pred. No. 1.7e-42;

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Best Local Similarity 90.4%; Pred. No. 6.7e-53;
Matches 253; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
Qy 1071 GGTAGAGAAATGTGATCATGCTGCTTGGTCTTTAAAGTTCTTTGGAGTGAAGTGTACTGAA 1130
Db 2 GGTAGAGAACGTGATCATGCTGCTTGGTCTTTAAAGTTCTTTGGAGTGAAGTGTACTGGA 61
Qy 1131 TTACTGTCAATCTCTTGGTCTTGCAGTCAATTTGCTTATCTGATTTCCATTGACTT 1190
Db 62 TTACTGTCAATCTCTTGCAGTCAATTTGCTTATCTGATTTCCATTGACTT 121
Qy 1191 CATGCTCTTTTCTTCCAGTCAATTTGCATCCATTTGGGCTCACTTTCCACCATAATGTAGT 1250
Db 122 CATGCTCTTTTCTTCCAGTCAATTTGCACCGCTGCTCACTTTCCACCACACGTAGT 181
Qy 1251 AGACTACCTTCATTTGCTGCTGTGCACAGCACCTCGGACAGGTTTGAGAACTCAGA 1310
Db 182 GGACTACCTACACTGTGTGCTGTGCATCAGCACCTCGGGCAGGGTTTGAGAACTCAGA 241
Qy 1311 GCCACCTTTTGAGACTGAAGCAAGGCAAGTGTCTGCTGA 1350
Db 242 GCCATCTGTTGATGCTGAACAAAGCAGACGATTTGCTGA 281

RESULT 7
LOCUS BI827782 881 bp mRNA linear EST 04-OCT-2001
DEFINITION 603075458F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5167070 5',
mRNA sequence.
ACCESSION BI827782
VERSION BI827782.1 GI:15939332
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 881)
NTH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1415 row: d column: 15
High quality sequence stop: 782.
FEATURES
Location/Qualifiers
1..881
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5167070"
/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."
BASE COUNT 257 a 163 c 194 g 266 t
ORIGIN

Query Match 14.7%; Score 198.8; DB 13; Length 881;
Best Local Similarity 57.3%; Pred. No. 1.7e-42;

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Matches 444; Conservative 0; Mismatches 313; Indels 18; Gaps 4;

Qy 46 GTTTTCATCTCTGGAGGAGATGTCATCGTGGAGCCACCCCGATTTACTTTTCCATTT 105
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Db 110 GTTTCATCTCTGGAAGAAGAAATAGTCTCTGG-CAGAGACTCCATTAAGTCTTCTTT 168
|||
Qy 106 AGCATCCTTTTCTCCACCTTTTGTACTGTGGGAGGCTGCATCTGCTTGTACATGTT 165
|||
Db 169 AGCATATCTCTCAACTGTTCTCTACTGTGTGAGGTGCTTGTGTATACATGTTT 228
|||
Qy 166 AGAATCTATCGAAGAAATAGTGAACCTTACCGGATGACATACACTTTTCTTCTTTATG 225
|||
Db 229 GAAATTTATCGAAGAAAGCTAATGACACATTTCTGGATGTCAITTTACCATCAGCTTTATTAT 288
|||
Qy 226 TTTTTCATCCATTTATGTCAGCTTCACTTCTTGTGACCTCAATTTTGTCCACAGAGCTAGCCAAAGAT 285
|||
Db 289 GTGGGGCAATTTTGGATCAAAATATCTCTGATGTTTTTCAACAAGAACTTGAGGAGAAAT 348
|||
Qy 286 AAACCGCTATCATTTATTTATGATCTAATCTCTTGGGACCTGTTTATCAGATGTTTGGAG 345
|||
Db 349 AAGGCTGCATTTACTTTTGTGGCAATTTCTTTTAGGACCTAATGAGGTGTTTGCAC 408
|||
Qy 346 GCCATGATTAAGTACCTCACACTGTGGAAGAAAGAGGAGGAGGCCCTATGTGAGC 405
|||
Db 409 ACCATTAGAAATTTACCACAAATGCTTGAATAATCTTAAACAGGAGAAAGAGACTCAA 468
|||
Qy 406 CTCACCGAAGAGAGTCTAATAGATGGCGAGAGGTGCTGTAGATGGAGGTGGC 465
|||
Db 469 GTTAGCATCAAGA-----GAAACACGATGCTGGAAGGGAGATTGCA 513
|||
Qy 466 CACTCATCCGACCCCTGGCTATGACCGCAATGCCTACAAACGTATGTACAGATCAA 525
|||
Db 514 TTCTCAATCCGGATAAATTTTCATGCAGAGAGGCTTTCAAGTACATGTCAATGATTCAG 573
|||
Qy 526 GCCTTCCTGGGCTCAGTGCCTCCAGCTCACCTATCAGCTCTATGTGAGCCTGATCTCTGCA 585
|||
Db 574 GCTTTTCTGGTCTGTTTCCACAATTAATTTTGCAGATGTATATCAGTCTCACTATACA 633
|||
Qy 586 GAGTTTCCCTGGTAGAGTTGCTAATGTATTTTCCCTGGTATCTGTGACCTATGGG 645
|||
Db 634 GAATGGCTTTGATAGAG-CATGCTGATGACATGTTCCCTGTTTATCAGTTACTTATGGG 692
|||
Qy 646 GCCACCTTTTGCATATGTTGGCTATCCAGATCAAGTACGATGACTACAGATTCGCTT 705
|||
Db 693 GCATTCGCTGCAATATACGTGGCATCCAGATCAGCAATGATATACCATATAAGCT 752
|||
Qy 706 GGCCCACTAGAAGTCTCT-GCATCACCATCTGCGGACATTTGAGATCACTTCCCGCT 764
|||
Db 753 ACCCGATAGAATTTCTGCTGCTGCTGCTGGGAGTATGGAAGTATCTCAGCTGGT 812
|||
Qy 765 CTGATTTCTGGTCTCTTCTCAGCACTTTGAAATGGAAGCTGTGCCCTTCTTA 819
|||
Db 813 AGTGACTCTGGCATTTTCCCTTGCATCTCTCAACTGTAGAGCTAAACCGTTGGTA 867
|||

RESULT 8
AA256009
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AA256009
zs28c06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686506 5',
mRNA sequence.
AA256009
AA256009.1 GI:1891549
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 201)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 1241 Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 183.
Location/Qualifiers
1. .201
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCGAAGTGGAGCGCGCTCATTTTCTTTTCTTTT-3',
1. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaudo."
BASE COUNT 39 a 46 c 36 g 80 t
ORIGIN
Query Match 14.7%; Score 197.8; DB 9; Length 201;
Best Local Similarity 99.0%; Pred. No. 1.8e-42;
Matches 199; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1077 GAATGTGATCATGCTCTGTTTAAAGTTTCTTTTGGAGTGAAGTGTACTGAATTAAGT 1136
Db 1 GAATGTGATCATGCTCTGTTTAAAGTTTCTATGGAGTGAAGTGTACTGAATTAAGT 60
Qy 1137 TCATTCCTGATTCGCTTCGAGCTCATTTGCTTATCTGATTTCCATGATTCATGCT 1196
Db 61 TCATTCCTGATTCGCTTCGAGCTCATTTGCTTATCTGATTTCCATTTGGCTCATGCT 120
Qy 1197 CCTTTTCTCCAGTACTTCGATCCATTCGCTCACTCTTACCCCATATGTAGTACTA 1256
Db 121 CCTTTTCTCCAGTACTTCGATCCATTCGCTCACTCTTACCCCATATGTAGTACTA 180
Qy 1257 CCTCCATTGCTGCTGCTGCA 1277
Db 181 CCTCCATTGCTGCTGCTGCA 201
RESULT 9
AL638533/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL638533
XGC-neurula Silurana tropicalis cDNA clone TNeu018n12 5',
mRNA sequence.
AL638533
AL638533.1 GI:16790512
EST.
western clawed frog.
Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 678)
Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger xenopus tropicalis EST project 2001

TROPICALIS SEQUENCE ID: TNeu018n12.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.

FEATURES

Location/Qualifiers
1..678
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TNeu018n12"
/clone_lib="XGC-neurula"
/lab_host="Escherichia coli DH10B"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dT primed from 5' of poly A+ RNA from neurula. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
225 a 156 c 153 g 144 t

BASE COUNT

ORIGIN
Query Match 14.3%; Score 193.4; DB 9; Length 678;
Best Local Similarity 58.7%; Pred. No. 4.3e-41;
Matches 335; Conservative 0; Mismatches 236; Indels 0; Gaps 0;
Qy 603 AGTTGTGTAATGGTATTTTCCCTGGTATCTGTCACTATGGGGCCACCCCTTTGCAATAT 662
Db 616 AGCTGCTCATGGCTATGTGCTTGGCTCAACTACATATGGTGCCTTAATCCTAATGT 557
Qy 663 GTTGCTATCCAGTCAAGTACGATGACTACAAAGATTCGCTTGGGCCACTAGAAATCCT 722
Db 556 CTTGCCCATACAAATTAAGTATGATGACTATAAAGTTCTGTAAGTGTGCCAGCGTTCCT 497
Qy 723 CTGCATACCACTCGGGACATCGAGATCACTTCCCGCCCTGATTCCTGCTCTT 782
Db 496 GTGCATGCTGATGGAGATGCTGGAGATGCTACCCGTTACAGTTCTGGTCTTTT 437
Qy 783 CTCAGCCACTTTGAATTAAGGCTGTGCCCTTCCCTAGTGTCTCAACTTCTGTATCATCT 842
Db 436 TTGTTCAAGCTTTAAGCCCTGGGTGCTGAGTGGCTTAGCAAACTTACTGGCGTCTT 377
Qy 843 CTTTGAGCCCTGGATTAAGTTCTGGAGAAAGTGGTGCCAGATGCCCAATAACATGAGAA 902
Db 376 CTTTGTGCTTGGTTAAATTTCTGGAGCAGTGGGACAGCTGCCCAACATAGAAAA 317
Qy 903 AAACCTTACGGCGTGGCAGCTGTGTGCTGCTGATTTAGTCACCATCTCTATGCTGG 962
Db 316 GAACCTTTAGCTGGTTTGGTACTGTGACAGTCTCTTGGGTGAGTAACCTTGTCTTATTCAGC 257
Qy 963 CATCAACTCTCTGCTGTGCTGAGTTGAGTTGGGACAGACAGATCTCGTCGA 1022
Db 256 CATCAATATGTTTGTGCTGCTGCTTCCAGCTAAACCTATCAGATCGGGAATTAATGA 197
Qy 1023 CAAAGGGCAGAACTGGGACATATGGGCTCGCACTATAGTGTGAGGTTGGTAGAGAAATGT 1082
Db 196 CCAGTCACAAACTGGGGAGGTTAAGTCTTCAATATACCACTCGGTGCTCGAGAAATGC 137
Qy 1083 GATCATGCTCTGGTTTAAAGTTCTTTGGAGTGAAGTGTGTACTGAATTAATGCTCATTC 1142
Db 136 AGCCCTCATCTGCTGCTGCTTCTACAGGAGGAGTGTGTTGAGTATTTCTGTTCCCC 77
Qy 1143 CTTGATTGCTTGGCAGTCAATATTGCTTTAT 1173
Db 76 ACTGCTGTGTTCAACTCTTAGTAGGATAT 46

RESULT 10
B1546216
LOCUS B1546216 793 bp mRNA linear EST 05-SEP-2001
DEFINITION 60318602F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5259961 5', mRNA sequence.
ACCESSION B1546216
VERSION B1546216.1 GI:15433528
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1. (bases 1 to 793)
NIH-MGC http://mgc.ncbi.nlm.nih.gov/.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM11655 row: c column: 02

High quality sequence stop: 707.

FEATURES

source

1..793
Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5259961"

/clone_lib="NIH_MGC_95"

/tissue_type="hippocampus"

/lab_host="DH10B"

/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to 500 ng. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 180 a 215 c 188 g 210 t

ORIGIN

Query Match 13.5%; Score 182.6; DB 13; Length 793;
Best Local Similarity 56.9%; Pred. No. 3.8e-38;
Matches 419; Conservative 0; Mismatches 304; Indels 14; Gaps 4;
Qy 250 ACCCTCATTTTGTCCACAGATCTAGCCAAAGATAAACCGCTATCATTTATTCAT 309
Db 1 AGCGGCTTCTTCGTACACCGCGACCTCAGCCGCGACCGCGCTCGTACTGCTGTCAC 60
Qy 310 CTAATCCTCTGGACCTGTATCAGATGTTGGAGGCCATGATTAAAGTACCTCACACTG 369
Db 61 CTGCTGCAACTTGGGCCCGTTTTCAGTGTGTTTGAAGTCTTCTGCACTCTAC----- 111
Qy 370 TGGAGAAAGAGAGAGCAGGAGGAGCCCTATGTCAGCCTCACCCGCAAGAGAG---ATGCTA 426
Db 112 TTTCAGTCAGGCAACAATCAAGAGCCTTATGTCAGTATCACCAAGAGAGGCAAAATGCCA 171
Qy 427 ATAGATGGCGAGAGGTGCTGTATAGAAATGGAGGTGGGCACCTCATCCGAGCCCTGGCT 486
Db 172 AAAAAATGGGCTCTCAGAGGAGATTGAGAAGAGGAGTGGGGCCAGAGCAAGCAAACTAATC 231
Qy 487 ATGCACCGCAATGCCCTACAAAGTATGTCACAGATCCAGACCTTCTCGGCTCAGTGCACC 546
Db 232 ACCACCGATCAGGTTTACGCCGGCGTCGGTGATCCAGGCTTCTTGGGCTCAGCCCC 291
Qy 547 CAGCTGACCTATCAGCTCTATGTAGCCCTGATCTCTGCAGAGGTTCCCTCGGTAGAGTT 606
Db 292 CAGCTGACCTACAGCTGTACATAAGTGTATGCAGCAGGACGTCACCTGTTGGAGAAGT 351
Qy 607 GTGCTAATGGTATTTCCCTGGTATCTGTCACTATGGGGCCACCCCTTTCGAATATGTTG 666
Db 352 CTCCTCATGACCATATCCCTGTTGTCCATTGTGTATGGAGCCTTGGGCTGCAACATCCTA 411
Qy 667 GCTATCCAGATCAAGTACCATGACTAC--AGATTCCCTTGGGGCCACTAGAACTCTCTG 725

```

Db 412 GCCATCAAAATCAAGTACGATGATGATGAAGTCAAGAGTGAAGCCCTCTGGCCCTATGCTG 471
Qy 726 CATACCACTCTGGCGACATTCGAGATCACTTCCCGCCCTCCGATTCGTGCTCTCTTC 785
Db 472 TATCTCTCTGTGGAGAGCTTTGAGATTGCCACTCGAGTTGATGCTCTGCTCTCTTTAC 531
Qy 786 ACCCACTTTGAAATTGAAGGCTGTGCGCCCTTCCTAGTGTCTCAACTTCTCTGATCATCTCTT 845
Db 532 CTCCTCTCTGAAGACCTGGCGGTGGTTATATACTACTCATCAACTTCTTCAGTTTCTCTTA 591
Qy 846 TGAGCCCTGGATTAGTTCTGAGAGAGTGGTGGCCAGATGCCAATAACATTGAGAAAAA 905
Db 592 GTACCCCTGGATCCCTCTCTGTGTGAGTGGTTCCTCCCATTCCTCGAACAATAGAG-AAGG 650
Qy 906 CTTAGCCGGGTGCGCACCTCTGTGTGCTGCTGATTTTCAGTCACCATCTCTATGCTGGCAT 965
Db 651 CCTAGTAGAGTGGGACACCACTTGTACTATGCTTAACTTCTACTCTACTACTGGGTA 710
Qy 966 CAACCTCTCTTCTGCTGT 982
Db 711 TTAACCATGTTCTCTGCT 727

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RESULT 11
AA791818 385 bp mRNA linear EST 09-FEB-1998
LOCUS v61c09_r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
DEFINITION IMAGE:1150768 5' similar to SW:KX_HUMAN P51811 MEMBRANE TRANSPORT
PROTEIN XK ; mRNA sequence.
ACCESSION AA791818
VERSION AA791818.1 GI:2854773
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 385)
REFERENCE
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Seftoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HMMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:623976
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 378.
Location/Qualifiers
FEATURES
source
1. .385
/organism="Mus musculus"
/strain="C57BL/6"
/db xref="taxon:10090"
/clone="IMAGE:1150768"
/clone_lib="Stratagene mouse skin (#937313)"
/sex="females"
/tissue types="whole skin"
/dev stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/notes="Organ: skin; Vector: pBluescript SK-; Site:1: EcoRI
; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5'
adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"

```

```

BASE COUNT 106 a 82 c 100 g 97 t
ORIGIN
Query Match 12.8%; Score 173.2; DB 9; Length 385;
Best Local Similarity 93.3%; Pred. No. 1e-35;
Matches 181; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy 416 AGAAGATGCTAATAGATGGCGAGGAGTCTGATAGAATGGGAGGTGGCCACTCCATCC 475
Db 1 AGAAGATGCTAATAGTCTGCCAGGAGGTCTGATAGAATGAAGGTGGGCACTCCATCC 60
Qy 476 GGACCTCTGCTATGCACCGCAATGCCCTACAAAGCTATGTACAGATCCCAAGCCTTCTCTGG 535
Db 61 GGACCTCTGCTATGCATCGCAATGCTCTACAAAGCTATGTACAGATCCCAAGCCTTCTCTGG 120
Qy 536 GCTCAGTCCCCAGCTGACCTATCAGCTCTATGTGAGCCTGATCTCTGAGAGGTTCCTCC 595
Db 121 GCTCAGTCCCCAGCTGACCTATCAGCTATATGTGATCTGATCTCTCAGCAGAGTCCCC 180
Qy 596 TGGGTAGAGTTCTGTG 609
Db 181 TGGGTAGAGGTGAG 194

RESULT 12
CNS02LHV CNS02LHV 691 bp DNA linear GSS 14-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION 147116 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL202756
VERSION AL202756.1 GI:7861101
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 691)
REFERENCE
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 691)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Unpublished
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 691)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.
FEATURES
source
1. .691
/organism="Tetraodon nigroviridis"
/db xref="taxon:99883"
/clone="147116"
/clone_lib="G"
/notes="Genoscope sequence ID : COAG147BE08LP1-end : T7"
BASE COUNT 128 a 182 c 187 g 189 t 5 Others
ORIGIN
Query Match 12.6%; Score 170.4; DB 17; Length 691;
Best Local Similarity 58.9%; Pred. No. 7.1e-35;

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Matches 305; Conservative 2; Mismatches 210; Indels 1; Gaps 1;

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Qy 590 TTCCCTGGGTAGAGTTGTGCTAATGGTATTTTCCTGGTATCTCTCACTATGGGCCA 649
Db 138 TGCTTCTGTTGGCATGGCTCTGATGATCATTAACCTGGTCTCCATCATACACGGGGTCT 197
Qy 650 CCCTTTGCAATATGTTGGCTATCCAGATCAAGTACGATGACTACAAAGATTCGCCCTTGGC 709
Db 198 TGGTGTGCRAGCTCTGGCCATCCATCATCAGTACGACGACTACAAAGGTGGG-GGTCCGC 256
Qy 710 CACTAGAAAGTCTCTGCATCAACCATCTCGCGGACATTTGGAGATCACTTCCCGCCCTCCGA 769
Db 257 CCCCGCCCTACCTGTGCATGACCGGTGGAGAGGGTTGGAGATCGCCACAGGATCACGG 316
Qy 770 TTTCTGGTCTCTCTCAGCCACTTTGAATTAAGAGGCTGTGCCCTTCTAGTGTCTCACT 829
Db 317 TTTCTGGTCTCTCTCAGCAGCGCTCAATATCTGGGTCTGCGCTCGCNCACCC 376
Qy 830 TCCTGATCATCTCTTTGAGCCCTGGATTAACTTCTGGAGAGTGTGCGCCAGATGCCCA 889
Db 377 TGCTTCTTCTTCTTCCAACTCTGACCGAGTTCTGGCCAAAGAGCTCGTTGACTC 436
Qy 890 ATAACTTTAGAGAAACTTTCAGCCGGTCTGGTCTCTGGTGGTCTCTGATTTTCAGTCACCA 949
Db 437 AGGCCCTGGAGCGAACTTCTCTCATTTTCGCGCACCGTGTGGTCTGAGCCTGTTTCAAGC 496
Qy 950 TCCTCTATGCTGGATCAACTTCTCTGCTGGTCTGAGCTTTGAGTGTGAGTTGGGAGACA 1009
Db 497 TGCTGTTTCGCTGCTGCTCAACGTGTTCTGCTGGTGGCGGTGCGAGCTTTCACCCACC 556
Qy 1010 GAGATCTCGTCAGAAAGGGGAGAGTCTGGGACATATGGCTCGACATATAGTGTGAGGT 1069
Db 557 GGGAGCTGATCCAGAGGAGGAGGCTGGGCGGAGTCTGCTCTGACTACTGCGCAGCT 616
Qy 1070 TGGTAGAGAAATGTCATGCTGCTTGGTCTTTTAAAGTTC 1107
Db 617 TCGTGGAGAACTTTGCTCTCATCAGCTGTGCTACTTC 654

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RESULT 13
BI463670
LOCUS 603207340P1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5273312 5',
DEFINITION mRNA sequence.
ACCESSION BI463670
VERSION BI463670.1 GI:15254326
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 855)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: csapbe-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11689 Row: 0 Column: 09
High quality sequence stop: 826.
Location/Qualifiers
1. 855
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/clone="IMAGE:5273312"
/clone_lib="NIH_MGC_97"

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5273312"
/clone_lib="NIH_MGC_97"

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); Oligo-dr primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 257 a 156 c 186 g 256 t
ORIGIN

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Query Match 12.2%; Score 164.6; DB 13; Length 855;
Best Local Similarity 57.0%; Pred. No. 2.8e-33;
Matches 329; Conservative 0; Mismatches 234; Indels 14; Gaps 1;
Qy 1 ATGGACAGAGTTTATGAATAATCTCTGAGGAGCCAAATGTGGATCCGGTTTCATCTCTGGAG 60
Db 104 ATGGACAGAGTTTGAAGAGATGATGAAGAAACACAGGAGGAGTTTCATCTCTCGAA 163
Qy 61 GAAGATGTCATCCGTTGGAGCCAAACCCCGATTTATCTTTCCATTTAGCATCTCTCTCC 120
Db 164 GAAGAAATAGTCTTGGCCAGAGACTCCATCTAAGCTTTCTCTTTAGCATTTATCTCTCA 223
Qy 121 ACCTTTGTACTGTGGGAGGCTGCTCTGTTTGTACATGTTAGATCTATCTCGAAAG 180
Db 224 ACTGTCTCTACTGTGGGAGGTTGCTTGGTTTATACATGTTTGAATTTTATCGAAA 283
Qy 181 AATAGTGAATACTACCGGATGACATACACCTTTCTTTCTTTATGTTTTCATCCATTATG 240
Db 284 GCTAATGACATCTGATGTCATTTACCATCAGCTTTATTTATTTGGGGGCAATTTTG 343
Qy 241 GTCCAGTTGACCCCTCAATTTTGTCCACAGATCTAGCCAAAGATAAACCGCTATCATTA 300
Db 344 GATCAAAATATCTGATGTTTTCACAAAGACTTGAGGAGAAATAAGCTGCTACTTACT 403
Qy 301 TTTATGATCTAATCTCTTGGGACCTGTTATCATGATTTTGGAGGCCATGATTAGTAC 360
Db 404 TTTTGGCAGATCTTCTTTTAGGACCTATTGAGGTTGTTGACACACCATTAAGAAATAC 463
Qy 361 CTCACATCTGTGGAAGAAAGAGGAGGAGGAGCCCTATGTGAGGCTCACCCGAAAGAAAG 420
Db 464 CACAAATGTTGAAAAATCTTAAACAGGAGAAAGAA-----GACTCAAG 509
Qy 421 ATGCTAATAGATGGCGAGGAGGTGCTGATAGAAATGGGAGGTGGGCCACATCCGACCC 480
Db 510 TTAGCATCAAAAGAGAAACACGATGCTGGCAAGGAGAGTTGCAATTTCTCAATCCGGAT 569
Qy 481 CTGGCTATGACCCGCAATGCCCTAGCAAGATGTCACAGATCCAAAGCCTTCTCTGGCTCA 540
Db 570 AATTTTCATGACGAGAGGCTTTTCAAGTACATGTGAGTGTGAGGCTTTCTCGGTTCT 629
Qy 541 GTGCCCCAGCTGACCTATCATGCTCTATGTGAGCCCTGA 577
Db 630 GTTCCACAAATTAATTTTGCAGATGATATCATGCTCA 666

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RESULT 14
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LOCUS AG085155 691 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-083B22.F, genomic survey sequence.
ACCESSION AG085155
VERSION AG085155.1 GI:16636957
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphoblast DNA, clone PTB-Chimpanzee Male
BAC library clone: PTB-083B22.F.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1
REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.

```

TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 691)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpbes@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB. This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS

Sequencing: -21M13

LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
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/db_xref="taxon:9598"
/clone="PTB-083B22.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT 230 a 151 c 127 g 181 t 2 others
ORIGIN

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Best Local Similarity 60.9%; Pred. No. 2e-19;
Matches 184; Conservative 0; Mismatches 118; Indels 0; Gaps 0;
QY 601 AGAGTTGCTAAATGGTATTTCCCTGGTATCTGTGACCTATGGGGCCACCTTTGCAAT 660
DB 354 ATAGCATTTGCTGATGACATGTTCCCTGTTATCAGTTACTTATGGGCCATTCGTCGAAT 295
QY 661 ATGTTGGCTATCCAGATCAAGTACGATGACTACAAGATTCGCCCTTGGGCCACTAGAATC 720
DB 294 ATACTGGCCATCCAGATCAGCAATGATGATGATCACTACCAAGCTACCGCCGATAGAAATTC 235
QY 721 CTCTGCATCACCATCTGGCGACATTTGAGATCACTTCCCGCCTCTGATTCGTGTCGTC 780
DB 234 TTCTGTGCTGATGTCGGCTTTTGGAGGTTATCTCAGCTGATGACTCTGCATTT 175
QY 781 TTCTGACCCACTTTGAATTAAGGCTGTGCGCTTCTCTAGTGTCTCAACTTCCCTGATCATC 840
DB 174 TTCATTGCATCTCTGAACTGAAGAGCTACCTTTTGTATCATATATTTTGTGCA 115
QY 841 CTCTTTGAGCCCTGGATTAAGTTCTGAGAAAGTGTGCGCCAGATGCCCAATAAATTGAG 900
DB 114 TTGTTGACACCGTGGCTGGAGTTTGGAAAAGTGAGGCTCGCGGAGCTGTCTAGTCGCG 55
QY 901 AA 902
DB 54 AA 53

RESULT 15
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LOCUS 603206970F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5272840 5',
DEFINITION mRNA sequence.
ACCESSION BI461092
VERSION BI461092.1 GI:15251748
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 666)

AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toehiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11688 row: k column: 17
High quality sequence stop: 663.

FEATURES
source

Location/Qualifiers
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/clone="IMAGE:5272840"
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/lab_hosts="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to ROI 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 125 a 212 c 197 g 132 t
ORIGIN

Query Match 8.0%; Score 107.6; DB 13; Length 666;
Best Local Similarity 53.5%; Pred. No. 6.3e-18;
Matches 277; Conservative 0; Mismatches 229; Indels 12; Gaps 2;
QY 118 TCCACCTTTTGTACTGGGGAGGCTGCATCTGCTTTGTATCATGTTAGATCATATCGA 177
DB 156 TCCGTGTTCTGTTGTCGGCGAGACAACGGCGCGCTCAGCCTGAGCAGCACCTACCGC 215
QY 178 AAGAAATAGTGAACCTTACCGGATGACATACACCTTTCTTTCTTTATGTTTTCATCCAT 237
DB 216 TCGGGCGGACCGCATGTGCGAGCGCTGACGTGCTTTTCTCGCTACTGCTTGC CG 275
QY 238 ATGCTCCAGTTGACCTCATTTTGTCCACAGAGATCTAGCCAAAGATAAACCCTATCA 297
DB 276 CTGTCGAGCTCAGCTTCTCTGTCACCGCGACCTCAGCCGCGCCGCTCGTA 335
QY 298 TTATTTATGATCTAATCTCTTTGGGACCTGTTATCAGATGTTTGGAGGCCATGATTAG 357
DB 336 CTGCTGTCGACCTGCTGCAACTTGGGCCCTTTTCAGGTGTTTGAAGTCTCTGTCATC 395
QY 358 TACCTCACACTGTGGAGAAGAGGAGCAGGAGGACCTATGTGTCAGCTCACCGGAAG 417
DB 396 TACTTTC-----AGTCAGGCAACAATGAAGAGCTTATGTGCTATCACCAGAAG 446
QY 418 A---AGATGCTAATAGATGGGAGGCTGCTAGATAGGAGTGGGCGACCTCCATC 474
DB 447 AGGCAATGCCAAAATAGGCTCTCAGAGAGATTTGAGAGAGGTGGCGCAGCAGAA 506
QY 475 CGGACCTGCTATGACCCGCAATGCTCAAAAGTATGTACAGATCCAAAGCCTTCCTG 534
DB 507 GGCAAACTAATACCCACCGATCAGCTTTCAGCCGGCGCTCGGTGATCCAGGCTTCTTG 566
QY 535 GGCCTAGTGGCCGAGCTGACCTATCAGCTCTATGTGAGCCCTGATCTCTGACAGAGTTCCC 594
DB 567 GGCTCAGCCGCCCGAGCTGACCTTACAGCTGTACATAAGTGTGCTATGACGAGGCTCACT 626
QY 595 CTGGGTAGAGTCTGCTTAATGTTATTTCCCTGGTATC 632
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